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1/77

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3. Full name, address and postcode of the or of each patent applicant *(underline all surnames)*

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Patents ADP number *(if you know it)*

If the applicant is a corporate body, give the country/state of its incorporation

7146961001

4. Title of the invention

NOVEL POLYPEPTIDES

5. Name of your agent *(if you have one)*

"Address for service" in the United Kingdom to which all correspondence should be sent *(including the postcode)*

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Patents ADP number *(if you know it)*

125001

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Country	Priority application number *(if you know it)*	Date of filing *(day / month / year)*

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a) any applicant named in part 3 is not an inventor, or

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11. I/We request the grant of a patent on the basis of this application.

Signature: Kilburn & Strode — Date: 24 November 1997

Kilburn & Strode

12. Name and daytime telephone number of person to contact in the United Kingdom

Martin P White
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Novel polypeptides

The present invention relates, *inter alia*, to novel desaturases and uses thereof.

Over the last few years a number of microsomal and soluble fatty acid desaturases have been isolated from higher plants, most notably *Arabidopsis thaliana*. This has resulted from a combined genetic and biochemical approach to the generation and complementation of mutant *Arabidopsis* lines defective in fatty acid desaturation or elongation [1]. The importance of this approach has been validated by the isolation and characterisation of genes encoding microsomal desaturases such the Δ^{12}[2] and Δ^{15}[3] desaturases (encoded by the FAD2 and FAD3 genes respectively), enzymes which had previously proved intractable to classical purification techniques on account of their hydrophobicity. The isolation of these and related genes, such as the Δ^{12} hydroxylase from *Ricinus communis* [4], has allowed the identification of a number of conserved motifs in plant microsomal desaturases, most notably the so called "histidine boxes" [5]. Proteins containing these motifs can be classified as di-iron centre-containing enzymes [6].

Recently a cDNA clone was isolated from borage, using highly degenerate PCR against these histidine motifs. This was shown by heterologous expression in transgenic tobacco to encode a microsomal Δ^6 desaturase [7]. Desaturation at the Δ^6 position is an unusual modification in higher plants, occurring only in a small number of species such as borage (*Borago officinalis*), evening primrose (*Oenothera spp.*) and redcurrant (*Ribes spp.*), which accumulate the Δ^6- unsaturated fatty acids γ-linolenic acid (GLA) and octadecatetraenoic acid (OTA) in the seeds and/or leaves.

GLA is a high value plant fatty acid, and is widely used in the treatment of a number of medical conditions, including eczema and mastalgia. It has been postulated that the

application of GLA replaces the loss of or meets an increased requirement for endogenous Δ^6 -unsaturated fatty acids [7]. The sequence of the borage microsomal Δ^6 desaturase differs from previously characterised plant microsomal desaturases/hydroxylases in that it contains an N-terminal extension which shows homology to cytochrome b_5, and also in that the third (most C-terminal) histidine box varies from the consensus [6] H-X-X-H-H, with a glutamine replacing the first histidine. This was also observed in the case of the cyanobacteria *Synechocystis* Δ^6 desaturase (GenBank ID; L11421).

Although Δ^6 fatty acid desaturation is an unusual modification in higher plants, it is believed to be common in animals. The essential fatty acid linoleic acid ($18:2\Delta^{9,12}$) is desaturated to GLA by a Δ^6 desaturase as a first step on the biosynthetic pathway of the eicosanoids (which include prostagladins and leucotrienes). This results in the rapid metabolism of GLA (to di-homo-GLA and arachidonic acid; i.e. $20:3\Delta^{8,11,14}$ and $20:4\Delta^{5,8,11,14}$ respectively). Accumulation of GLA is therefore not usually observed.

According to the present invention, there is provided a polypeptide having desaturase activity, which comprises the amino acid sequence shown in Figure 1.

The amino acid sequence shown in Figure 1 is in respect of a Δ^6 desaturase that is present in the nematode worm *Caenorhabditis elegans*. This is highly significant since prior to the present invention no successful sequencing or purification of an animal Δ^6 desaturase had been reported.

The amino acid sequence shown in Figure 1 is also of significance because it has a very low level of sequence identity with the borage Δ^6 desaturase (the only other eukaryotic Δ^6 desaturase to have been sequenced prior to the present invention). Indeed, this level of sequence identity is below 32 %. At such a low level of identity it might be expected that

the two polypeptides would have completely different functions. Unexpectedly, both have Δ^6 desaturase activity.

The present invention is however not limited to the Δ^6 desaturase having the sequence shown in Figure 1. It also includes other desaturases having at least 32% sequence identity therewith. Preferred polypeptides of the present invention have at least 40 % or at least 50% amino acid sequence identity therewith. More preferably the degree of sequence identity is at least 75%. Sequence identities of at least 90%, at least 95% or at least 99% are most preferred.

For the purposes of the present invention sequence identity (whether amino acid or nucleotide) can be determined by using the "BESTFIT" program of the Wisconsin Sequence Analysis Package GCG 8.0.

Where high degrees of sequence identity are present there may be relatively few differences in amino acid sequence. Thus for example there may be less than 20, less than 10, or even less than 5 differences.

Fragments of the polypeptides described above are also within the scope of the present invention, provided that they have desaturase activity. These are at least 100 amino acids long.

In summary, a polypeptide of the present invention has desaturase activity and:

a) comprises the amino acid sequence shown in Figure 1;

b) has one or more amino acid deletions, insertions or substitutions relative to a polypeptide as defined in a) above, but has at least 32% amino acid sequence identity therewith; or

c) is a fragment of a polypeptide as defined in a) or b) above, which is at least 100 amino acids long.

[The term "polypeptide" is used herein in a broad sense to indicate that a particular molecule comprises a plurality of amino acids joined together by peptide bonds. It therefore includes within its scope substances, which may sometimes be referred to in the literature as peptides, polypeptides or proteins.]

Desirably a polypeptide of the present invention will have a cytochrome domain. A cytochrome domain can be defined as an electron-transporting domain that contains a heme prosthetic group. Preferably a cytochrome b domain is present. More preferably a cytochrome b_5 domain is present (desirably this includes the H-P-G-G motif). A cytochrome b_5 domain is present in both the borage 6 desaturase and in the *C. elegans* 6 desaturase amino acid sequence shown in Figure 2B. The cytochrome b_5 domain is preferably an N-terminal domain – i.e. it is closer to the N-terminal end of the desaturase than to the C-terminal end. This contrasts with borage 6 desaturase, which has a C-terminal cytochrome b_5 domain.

A polypeptide of the present invention preferably has one or more (e.g. three) histidine boxes. One of these may have an H→Q substitution. (This provides a variant histidine box that is believed to be conserved over a range of animal / plant species.)

Polypeptides of the present invention can have any type of desaturase activity, although it is preferred that they are front end desaturases that introduce a double bond between the C3 and C7 positions, measured from the COOH group. A skilled person is readily able to distinguish between different desaturases by determining the different positions of double bonds introduced by the desaturases. This can be done by known analytical techniques e.g. by using gas chromatography. Particularly preferred desaturases are Δ^6 desaturases.

Desirably the desaturases occur naturally in one or more organisms that do not accumulate GLA (i.e. where GLA may be produced, but is not normally detectable

because it is very quickly metabolised). Such desaturases may occur naturally in one or more animals. Preferred desaturases occur naturally in one or more nematodes, e.g. in *C. elegans*.

In order to appreciate the scope of the present invention more fully, polypeptides within the scope of each of a), b) and c) above will now be discussed in greater detail.

Polypeptides within the scope of a)

A polypeptide within the scope of a) may consist of the amino acid sequence shown in Figure 1 or may have an additional N-terminal and/or an additional C-terminal amino acid sequence.

Additional N-terminal or C-terminal sequences may be provided for various reasons and techniques for providing such additional sequences are well known in the art. Such techniques include using gene-cloning techniques whereby nucleic acid molecules are ligated together and are then used to express a polypeptide in an appropriate host.

Additional sequences may be provided in order to alter the characteristics of a particular polypeptide. This can be useful in improving expression or regulation of expression in particular expression systems. For example, an additional sequence may provide some protection against proteolytic cleavage.

Additional sequences can also be useful in altering the properties of a polypeptide to aid in identification or purification. For example, a signal sequence may be present to direct the transport of the polypeptide to a particular location within a cell or to export the polypeptide from the cell. Different signal sequences can be used for different expression systems.

Another example of the provision of an additional sequence is where a polypeptide is linked to a moiety capable of being isolated by affinity chromatography. The moiety

may be an epitope and the affinity column may comprise immobilised antibodies or immobilised antibody fragments that bind to said epitope (desirably with a high degree of specificity). The resultant fusion protein can usually be eluted from the column by addition of an appropriate buffer.

Additional N-terminal or C-terminal sequences may, however, be present simply as a result of a particular technique used to obtain a substance of the present invention and need not provide any particular advantageous characteristic.

Polypeptides within the scope of b)

Turning now to the polypeptides defined in b) above, it will be appreciated that these are variants of the polypeptides given in a) above.

Various changes can often be made to the amino acid sequence of a polypeptide which has a desired property in order to produce variants which still have that property. Such variants of the polypeptides described in a) above are within the scope of the present invention and are discussed in greater detail in sections *(i)* to *(iii)* below. They include allelic and non-allelic variants.

(i) Substitutions

An example of a variant of the present invention is a polypeptide as defined in a) above, apart from the substitution of one or more amino acids with one or more other amino acids.

The skilled person is aware that various amino acids have similar characteristics. One or more such amino acids of a polypeptide can often be substituted by one or more other such amino acids without eliminating a desired property of that polypeptide (such as desaturase activity).

For example, the amino acids glycine, alanine, valine, leucine and isoleucine can often be substituted for one another (amino acids having aliphatic side chains). Of these possible substitutions it is preferred that glycine and alanine are used to substitute for one another (since they have relatively short side chains) and that valine, leucine and isoleucine are used to substitute for one another (since they have larger aliphatic side chains which are hydrophobic). Other amino acids that can often be substituted for one another include phenylalanine, tyrosine and tryptophan (amino acids having aromatic side chains); lysine, arginine and histidine (amino acids having basic side chains); aspartate and glutamate (amino acids having acidic side chains); asparagine and glutamine (amino acids having amide side chains); and cysteine and methionine (amino acids having sulphur containing side chains).

Substitutions of this nature are often referred to as "conservative" or "semi-conservative" amino acid substitutions.

(ii) Deletions

Amino acid deletions can be advantageous since the overall length and the molecular weight of a polypeptide can be reduced whilst still retaining a desired activity. This can enable the amount of polypeptide required for a particular purpose to be reduced.

(iii) Insertions

Amino acid insertions relative to a polypeptide as defined in a) above can also be made. This may be done to alter the nature of the polypeptide (e.g. to assist in identification, purification or expression).

Polypeptides incorporating amino acid changes (whether substitutions, deletions or insertions) relative to the sequence of a polypeptide as defined in a) above can be provided using any suitable techniques. For example, a nucleic acid sequence incorporating a desired sequence change can be provided by site-directed mutagenesis.

This can then be used to allow the expression of a polypeptide having a corresponding change in its amino acid sequence.

Polypeptides within the scope of c)

As discussed *supra*, it is often advantageous to reduce the length of a polypeptide. Feature c) of the present invention therefore covers fragments of the polypeptides a) or b) above which are at least 100 amino acids long, but which do not need to be as long as the full length polypeptide shown in Figure 1. Desirably these fragments are at least 200, at least 300 or at least 400 amino acids long.

Various uses of the polypeptides of the present invention will now be described.

Polypeptides of the present invention may be used, *inter alia* , in obtaining useful metabolites . For example Δ^6 desaturases can be used in obtaining gamma linolenic acid (GLA) or in obtaining metabolites in respect of which GLA is a precursor. For example, octadecatetraenoic acid (OTA; $18{:}4\Delta^{6,9,12,15}$) may be produced by the Δ^6-desaturation of alpha-linolenic acid.

Such metabolites are useful in medicine. They can be used in the preparation of a medicament for treating a disorder involving a deficiency in GLA or of a metabolite derived *in vivo* from GLA (e.g. an eicosanoid). Disorders which may be treated include eczema, mastalgia, hypercholesterolemia, atherosclerosis, coronary disease, diabetic neuropathy, viral infections and cancer.

The metabolites may be produced *in vivo* in non-human hosts or *in vitro*.

When a metabolite is to be produced *in vitro,* a desaturase of the present invention and its substrate will normally be provided separately and then combined when it is desired to

produce the metabolite. The present invention therefore includes within its scope a method of making GLA comprising using a Δ^6 desaturase of the present invention to convert a linoleic acid substrate to GLA.

When a metabolite is to be produced *in vivo* in a non-human organism, the substrate for a desaturase of the present invention will normally be provided by the relevant non-human organism itself. *In vivo* production of the metabolite can therefore be achieved by inserting a gene encoding a desaturase of the present invention into the organism and allowing the organism to express the desaturase. The desaturase can then act on its substrate. It will therefore be appreciated that polypeptides of the present invention can be used to provide desaturase activity in organisms that would normally not possess such activity or to increase the level of desaturase activity in organisms already having some desaturase activity. If desired, a useful metabolite may be purified from such an organism. Alternatively the organism itself may be used directly as a source of the metabolite. Particular cloning techniques that can be used to provide transgenic organisms with desaturase activity are discussed later on.

Polypeptides of the present invention can also be used as indicators of the transformation of an organism. For example, if an organism intended to be transformed does not have a particular desaturase and a nucleic acid intended for use in transformation encodes that desaturase, an assay can be performed after attempted transformation to determine whether or not the desaturase is present. Thus, in the case of the Δ^6 desaturase, an assay for the presence of GLA may be performed and GLA can serve as a simple marker for the presence of a transgene cassette comprising a Δ^6 desaturase encoding sequence.

A further use of the present invention is in providing antibodies. The present invention includes within its scope antibodies that bind to polypeptides of the present invention.

Preferred antibodies bind specifically to polypeptides of the present invention and can therefore be used to purify such polypeptides. (For example, they may be immobilised and used to bind to polypeptides of the present invention. The polypeptides may then be eluted by washing with a suitable eluent under appropriate conditions.)

An antibody or a derivative thereof within the scope of the present invention may be used in diagnosis. For example binding assays using such an antibody or a derivative can be used to determine whether or not a particular desaturase is present. This is useful in diagnosing disorders that arise due to the absence of the functional desaturase.

Antibodies within the scope of the present invention may be monoclonal or polyclonal.

Polyclonal antibodies can be raised by stimulating their production in a suitable animal host (e.g. a mouse, rat, guinea pig, rabbit, sheep, goat or monkey) when a polypeptide of the present invention is injected into the animal. If necessary an adjuvant may be administered together with a polypeptide of the present invention. The antibodies can then be purified by virtue of their binding to a polypeptide of the present invention.

Monoclonal antibodies can be produced from hybridomas. These can be formed by fusing myeloma cells and spleen cells which produce the desired antibody in order to form an immortal cell line. Thus the well-known Kohler & Milstein technique (*Nature* **256** 52-55 (1975)) or variations upon this technique can be used.

Techniques for producing monoclonal and polyclonal antibodies that bind to a particular polypeptide are now well developed in the art. They are discussed in standard immunology textbooks, for example in Roitt *et al*, *Immunology* second edition (1989), Churchill Livingstone, London.

In addition to whole antibodies, the present invention includes derivatives thereof which are capable of binding to polypeptides of the present invention. Thus the present

invention includes antibody fragments and synthetic constructs. Examples of antibody fragments and synthetic constructs are given by Dougall *et al* in *Tibtech* **12** 372-379 (September 1994).

Antibody fragments include, for example, Fab, $F(ab')_2$ and Fv fragments. (These are discussed, for example, in Roitt *et al* [*supra*].) Fv fragments can be modified to produce a synthetic construct known as a single chain Fv (scFv) molecule. This includes a peptide linker covalently joining V_h and V_l regions, which contributes to the stability of the molecule. Other synthetic constructs that can be used include CDR peptides. These are synthetic peptides comprising antigen-binding determinants. Peptide mimetics may also be used. These molecules are usually conformationally restricted organic rings that mimic the structure of a CDR loop and that include antigen-interactive side chains.

Synthetic constructs include chimaeric molecules. Thus, for example, humanised (or primatised) antibodies or derivatives thereof are within the scope of the present invention. An example of a humanised antibody is an antibody having human framework regions, but rodent hypervariable regions.

Synthetic constructs also include molecules comprising an additional moiety which provides the molecule with some desirable property in addition to antigen binding. For example the moiety may be a label (e.g. a fluorescent or radioactive label). Alternatively, it may be a pharmaceutically active agent.

The present invention also includes nucleic acid molecules within its scope.

Such nucleic acid molecules:

a) code for a polypeptide according to the present invention; or

b) are complementary to molecules as defined in a) above; or

c) hybridise to molecules as defined in a) or b) above.

These nucleic acid molecules and their uses are discussed in greater detail below:

The polypeptides of the present invention can be coded for by a large variety of nucleic acid molecules, taking into account the well-known degeneracy of the genetic code. All of these coding nucleic acid molecules are within the scope of the present invention. Preferred coding nucleic acid molecules encode the polypeptide shown in Figure 1. These include nucleic acid molecules comprising the coding sequence shown in Figure 1 and degenerate variants thereof.

The nucleic acid molecules may be used directly. Alternatively they may be inserted into vectors.

Nucleic acids or vectors containing them may be used in cloning. They may be introduced into non-human hosts to enable the expression of polypeptides of the present invention using techniques known to those skilled in the art. Alternatively, cell free expression systems may be used.

Techniques for cloning, expressing and purifying polypeptides are well known to the skilled person. Various such techniques are disclosed in standard text-books, such as in Sambrook *et al* [*Molecular Cloning* 2nd Edition, Cold Spring Harbor Laboratory Press (1989)]; in Old & Primrose [*Principles of Gene Manipulation,* 5th Edition, Blackwell Scientific Publications (1994); and in Stryer [*Biochemistry,* 4th Edition, W H Freeman and Company (1995)].

By using an appropriate expression system the polypeptides can be produced in a desired form. For example, the polypeptides can be produced by micro-organisms such as bacteria or yeast, by cultured insect cells (which may be baculovirus-infected), or by mammalian cells (such as CHO cells).

However preferred hosts are plants or plant propagating material e.g. oil seed rape, sunflower, cereals including maize, tobacco, legumes including peanut and soybean, safflower, oil palm, coconut and other palms, cotton, sesame, mustard, linseed, castor, borage and evening primrose, or propagating material therefor.

The technology for providing plants or plant propagating material is now well developed. It is briefly discussed in WO 96/21022, for example.

Particular techniques that can be used are discussed below. It will of course be appreciated that such techniques are non-limiting.

(i) Vector systems based on Agrobacterium tumefaciens.

These include Ti based systems, such as pGV3850, in which the T-DNA has been disarmed. Desirably a selectable marker is present (e.g. a marker that provides resistance to an antibiotic).

Intermediate vectors (IVs) may also be used. They tend to be small in size and are therefore usually easier to manipulate than large Ti based vectors. IVs are generally vectors resulting from T-DNA having been cloned into *E. coli* derived plasmid vectors, such as pBR322. IVs are often conjugation-deficient and therefore a conjugation-proficient plasmid (such as pRK2013) may be used to mobilise an IV so that it can be transferred to an *Agrobacterium* recipient. *In vivo* homologous recombination can then occur in an *Agrobacterium* to allow an IV to be inserted into a resident, disarmed Ti plasmid in order that a cointegrate can be produced that is capable of replicating autonomously in the *Agrobacterium*.

Another alternative is to use binary Ti vectors. Here a modified T-DNA region carrying foreign DNA can be provided on a small plasmid that replicates in *E. coli* (e.g. pRK252). This plasmid (sometimes called mini-Ti or micro-Ti) can then be transferred

conjugatively via a tri-parental mating into an *A. tumefaciens* that contains a compatible *vir* gene (providing the *vir* function in *trans*).

Binary vectors without Ti sequences may even be used. Here bacterial *mob* and *oriT* functions may be used to promote plasmid transfer. Again, the *vir* function may be provided in *trans* .

The vector systems discussed above can be used to transfer genes into plants by using the protocol of Horsch *et al.* (*Science* **227**, 1229-31 (1985)) or variants thereof. Here small discs can be punched from the leaves of a dicotyledenous plant, they can be surface-sterilised, and can then be placed in a medium including *A. tumefaciens* that contains recombinant T-DNA in which a foreign gene to be transferred is accompanied by a selectable marker (e.g. the *neo* gene). The discs can then be cultured for 2 days and then transferred to a medium for selecting the selectable marker. (This can be done for a *neo* selectable marker by culturing using a medium containing kanamycin). *A. tumefaciens* can be killed by using a carbenicillin containing medium. Shoots will normally develop from a callus after 2-4 weeks. They can then be excised and transplanted to root-inducing medium and, when large enough can be transplanted into soil.

(ii) Vector systems based on Agrobacterium rhizogenes

These include Ri derived plasmids. Ri T-DNA is generally considered not to be deleterious and therefore such plasmids can be considered as equivalent to disarmed Ti plasmids. An IV co-integrate system based on Ri plasmids has been developed.

(iii) Plant protoplast based transformation systems

Transformation of plants can be facilitated by removing plant cell walls to provide protoplasts. The cell walls can be removed by any suitable means, including mechanical disruption or treatment with cellulolytic and pectinolytic enzymes. Protoplasts can then be separated from other components by centrifugation and techniques such as electroporation can then be used to transform the protoplasts with heterologous DNA.

Under appropriate culture conditions the transformed protoplasts will grow new cell walls and also divide. Shoots and roots can then be induced and plantlets formed.

(iv) Transfection by biolistics

High velocity microprojectiles carrying DNA or RNA can be used to deliver that DNA or RNA into plant cells. This has allowed a wide variety of transgenic plants to be produced and is suitable for both monocotyledenous and dicotyledenous plants. For example gold or tungsten particles coated with DNA or RNA can be used. Suitable devices for propelling the microprojectiles include gunpowder based devices, electric discharge based devices and pneumatic devices.

(v) Virus based systems

DNA plant virus vectors include cauliflower mosaic viruses (which infect a range of dicots.) and geminiviruses (which infect a wide range of dicots. and monocots.).RNA plant viruses are in the majority and include Brome Mosaic Virus (which infects a number of *Graminae*, including barley) and Tobacco Mosaic Virus (which infects tobacco plants).

From the foregoing description it will be appreciated that nucleic acid molecules encoding polypeptides of the present invention can be cloned and expressed in a wide variety of organisms.

In addition to nucleic acid molecules coding for polypeptides of the present invention (referred to herein as "coding" nucleic acid molecules), the present invention also includes nucleic acid molecules complementary thereto. Thus, for example, both strands of a double stranded nucleic acid molecule are included within the scope of the present invention (whether or not they are associated with one another). Also included are mRNA molecules and complementary DNA molecules (e.g. cDNA molecules).

Nucleic acid molecules that can hybridise to one or more of the nucleic acid molecules discussed above are also covered by the present invention. Such nucleic acid molecules are referred to herein as "hybridising" nucleic acid molecules.

A hybridising nucleic acid molecule of the present invention may have a high degree of sequence identity along its length with a nucleic acid molecule within the scope of a) or b) above (e.g. at least 50%, at least 75% or at least 90% sequence identity).

As will be appreciated by those skilled in the art, the greater the degree of sequence identity that a given single stranded nucleic acid molecule has with another single stranded nucleic acid molecule, the greater the likelihood that it will hybridise to a single stranded nucleic acid molecule which is complementary to that other single stranded nucleic acid molecule under appropriate conditions.

Desirably hybridising molecules of the present invention are at least 10 nucleotides in length and preferably are at least 25, at least 50, at least 100 nucleotides or at least 200 in length.

Preferred hybridising molecules hybridise under stringent hybridisation conditions. One example of stringent hybridisation conditions is where attempted hybridisation is carried out at a temperature of from about 35°C to about 65°C using a salt solution that is about 0.9 molar. However, the skilled person will be able to vary such parameters as appropriate in order to take into account variables such as probe length, base composition, type of ions present, etc.

Most preferably, hybridising nucleic acid molecules of the present invention hybridise to a DNA molecule having the coding sequence shown in Figure 1 to an RNA equivalent thereof, or to a complementary sequence to either of the aforesaid molecules.

Hybridising nucleic acid molecules can be useful as probes or primers, for example.

Probes can be used to purify and/or to identify nucleic acids. For example they can be used to identify the presence of all or part of a desaturase gene and are therefore useful in diagnosis.

Primers are useful in amplifying nucleic acids or parts thereof, e.g. by PCR techniques.

In addition to being used as probes or primers, hybridising nucleic acid molecules of the present invention can be used as antisense molecules to alter the expression of polypeptides of the present invention by binding to complementary nucleic acid molecules. (Generally this can be achieved by providing nucleic acid molecules that bind to RNA molecules that would normally be translated, thereby preventing translation due to the formation of duplexes.)

Hybridising molecules may also be provided as ribozymes. Ribozymes can also be used to regulate expression by binding to and cleaving RNA molecules that include particular target sequences recognised by the ribozymes.

From the foregoing discussion it will be appreciated that a large number of nucleic acids are within the scope of the present invention. Unless the context indicates otherwise, nucleic acid molecules of the present invention may therefore have one or more of the following characteristics:

1) They may be DNA or RNA (including variants of naturally occurring DNA or RNA structures, which have non-naturally occurring bases and/or non-naturally occurring backbones).
2) They may be single or double stranded.
3) They may be provided in recombinant form i.e. covalently linked to a heterologous 5' and/or 3' flanking sequence to provide a chimaeric molecule (e.g. a vector) which does not occur in nature.

4) They may be provided without 5' and/or 3' flanking sequences that normally occur in nature.

5) They may be provided in substantially pure form, e.g. by using probes to isolate cloned molecules having a desired target sequence or by using chemical synthesis techniques. Thus they may be provided in a form which is substantially free from contaminating proteins and/or from other nucleic acids.

6) They may be provided with introns (e.g. as a full-length gene) or without introns (e.g. as cDNA).

The present invention will now be described by way of example with reference to the accompanying drawings, wherein:

Fig 1 shows the DNA sequence and the deduced amino acid sequence of the full length *C. elegans* cDNA pCeD6.1. The positions of the N-terminal cytochrome b_5 domain and the variant third histidine box are underlined. The deduced amino acid sequence of this cDNA is identical to that predicted for residues 1-38 and 68-473 of W08D2.4.

Fig 2A shows a comparison of the deduced amino acid sequences of the *C. elegans* cDNA CeD6.1 and the *C. elegans* predicted protein W08D2.4. (MywormD6=CeD6.1; cew08d2=ORF W08D2.4.)

Fig 2B shows a comparison of the deduced amino acid sequences of the borage Δ^6 desaturase [7] and the *C. elegans* cDNA CeD6.1. (MywormD6=CeD6.1; Bodes6=borage Δ^6 desaturase.)

Fig 3 shows methyl esters of total lipids of *S. cerevisiae* grown under inducing conditions (linololate and galactose). Panel A is yeast transformed with control (empty) vector pYES2, panel B is transformed with pYCeD6.1. The common fatty

acid-methyl esters were identified as 16:0 (peak 1), 16:1 (peak 2), 18:0 (peak 3), 18:1 (peak 4), 18:2 (peak 5; supplied exogenously). The additional peak (6) in panel B corresponds to 18:3 GLA, and is indicated by an arrowhead.

Fig 4 shows GC-MS analysis of the novel peak identified in yeast carrying pYCeD6.1. The sample was analyzed for mass spectra as before [7], and the data used to search a library of profiles. The sample was identified as GLA. A comparison of the mass spectra of the novel peak (A) and authentic GLA (B) is shown; visual and computer-based inspection revealed them to be identical.

Fig 5 shows a simplified version of the metabolism of n-6 essential fatty acids in mammals. It can be seen that gamma-linolenic acid is an intermediate in the formation of arachidonic acid. Arachidonic acid is useful as a precursor of various eicosanoids (including prostaglandins and leucotrienes).

Materials & Methods

The NCBI EST sequence database was searched for amino acid sequences using a known borage Δ^6 fatty acid desaturase [7] and limiting the search to sequences containing a variant histidine box Q-X-X-H-H.

C. elegans ESTs were identified. They were further characterised by searching the *C. elegans* EST project database (Y. Kohara lab; DNA Data base of Japan) to identify related cosmid clones.

A partial cDNA clone identified by these searches was obtained from the *C. elegans* EST project (Prof Y Kohara, Japan), and this was used to screen a *C. elegans* cDNA library (mixed stage; also supplied by Prof Kohara). A number of positives were

identified and further purified, and full length clones were confirmed by sequencing to encode a transcript likely to have been transcribed from the gene designated W08D2.4, on cosmid W08D2, as determined by database searching of the genes sequenced by the *C. elegans* genome project.

The coding sequence of W08D2.4 was introduced into the yeast expression vector pYES2 by PCR. Oligonucleotides with 5' overhangs were used to introduce *Kpn*I and *Sac*I sites at the 5' and 3' ends respectively. The fidelity of the construct was checked by *in vitro* transcription and translation using the TnT system (Promega).

The resulting plasmid was introduced into yeast (*S. cerevisiae*) by the lithium acetate method [9], and expression of the transgene was induced by the addition of galactose. The yeast was supplemented by addition of 0.2 mM linoleate (sodium salt) in the presence of 1% tergitol NP-40.

Yeast total fatty acids were analyzed by GC of methyl esters [7]. Confirmation of the presence of GLA was carried out by GC-MS [7].

Results.

Our searches of EST databases identified a *C. elegans* EST, designated as yk436b12.

This partial sequence of 448 bases was used to search for related cosmid clones sequenced by the *C. elegans* genome project, using the DNA database of Japan *C. elegans* EST project server. This indicated that the clone yk436b12 was homologous to part of a gene present on cosmid W08D2 (Genbank accession number Z70271), which forms part of chromosome III [10]. Bases 21-2957 of cosmid W0D2 are predicted by the protein prediction programme Genefinder [10] to encode an ORF of 473 residues which is interrupted by 5 introns.

Examination of this predicted polypeptide (designated W08D2.4 by the Sanger Centre Nematode Sequencing Project, Hinxton, UK) revealed that it had a number of characteristics reminiscent of a microsomal fatty acid desaturase, including three histidine boxes. However, the predicted protein sequence indicated the presence of an N-terminal domain similar to cytochrome b_5, containing the diagnostic H-P-G-G motif found in cytochrome b_5 proteins [11]. Since the Δ^6 desaturase isolated by us from borage [7] also contained an N-terminal b_5 domain, this indicated that W0D2.4 may encode a Δ^6 desaturase.

Closer examination of the sequence revealed the presence of the variant third histidine box, with an H→Q substitution (again as observed in the borage Δ^6 desaturase). The degree of similarity between W08D2.4 and the borage Δ^6 desaturase is <52% and is therefore low. The figure of <31% obtained for identity is also low.

Since W08D2.4 was encoded by a gene containing many (6) introns, it was necessary to isolate a full length cDNA to verify the sequence predicted by the Genefinder programme [10], and to also allow the expression of the ORF to define the encoded function.

A cDNA library and EST yk436b12 were generously provided by Prof Y. Kohara (National Institute of Genetics, Mishima, Japan) and a number of positive plaques were identified by screening with the EST insert. These were further purified to homogeneity, excised, and the largest inserts (of ~1450 bp) from the resulting rescued phagemids were sequenced. This confirmed that the cDNAs isolated by us were indeed homologous to W08D2.4, with the 5' and 3' ends of the cDNA being equivalent to bases 9 and 3079 of the sequence of cosmid W08D2. Since the ATG initiating codon predicted by the Genefinder programme to be the start of gene product W08D2.4 was indeed the first methionine in the cDNA clone, we reasoned that we had

isolated a *bona fide* full length cDNA. The DNA sequence and deduced amino acid sequence of one representative cDNA clone (termed pCeD6.1; 1463 bp in length) is shown in Fig 1; the deduced amino acid sequence is identical to that predicted for W08D2.4 over the majority of the protein.

However, DNA sequences encoding residues 38-67 (Y-S-I.....L-Y-F) predicted for W08D2.4 are not present in the cDNA clone. This means that the deduced amino acid sequence of CeD6.1 is in fact 443 amino acids long, as opposed to that predicted for W08D2.4, which is 473 residues in length. The only other difference between the two amino acid sequences is an M→V substitution at residue 401, resulting from an A→G base change (base 1211). The two sequences are compared in Fig 2A, as is the deduced amino acid sequence of the borage Δ^6 desaturase and that of CeD6.1 (Fig 2B). The extra sequence predicted for W08D2.4 is likely to derived from incorrect prediction of intron-exon borders.

Note the presence of the H-P-G-G cytcochrome b_5 motif in the N-terminus (encoded by bases 96-108) and the H Q substitution in the third histidine box (encoded by bases 1157-1172).

Clone pCeD6.1 was then used as a template for PCR amplification of the entire predicted coding sequence (443 amino acid residues in length), and cloned into the yeast expression vector pYES2 (Invitrogen) to yield pYCeD6. The fidelity of this PCR-generated sequence was checked *in vitro* transcription/translation of the plasmid, using the T7 RNA polymerase promoter present in pYES2.

Using the Promega TnT coupled transcription/translation system,translation products were generated and analysed by SDS-PAGE and autoradiography as per the manufacturer's instructions. This revealed (data not shown) that the plasmid pYCeD6

generated a product of ~55kD, whereas the control (pYES2) failed to yield any protein products, indicating that the construct was correct.

Transformation and selection of yeast able to grow on uracil-deficient medium revealed yeast colonies carrying the recombinant plasmid pYCeD6 by virtue of the URA3 selectable marker carried by pYES2. Expression of pYCeD6 was obtained by inducing the GAL promoter that is present in pYES2. This was carried out after the cells had been grown up overnight with raffinose as a carbon source, and the medium supplemented by the addition of linoleate (18:2) in the presence of low levels of detergent. This later addition was required since the normal substrate for Δ^6 desaturation is 18:2 fatty acids, which do not normally occur in *S. cerevisiae*.

The cultures were then allowed to continue to grow after induction, with aliquots being removed for analysis by GC. When methyl esters of total fatty acids isolated from yeast carrying the plasmid pYCeD6 and grown in the presence of galactose and linoleate were analyzed by GC, an additional peak was observed (Fig 3). This had the same retention time as an authentic GLA standard, indicating that the transgenic yeast were capable of Δ^6-desaturating linoleic acid. No such peaks were observed in any of the control samples (transformation with pYES2). The identity of this extra peak was confirmed by GC-MS, which positively identified the compound as GLA (Fig 4). This confirms that CeD6.1 encodes a *C. elegans* Δ^6 desaturase, and that this cDNA is likely to be transcribed from the gene predicted to encode ORF W08D2.4, though the deduced amino acid sequence of CeD6.1 is 30 residues smaller than that of W08D2.4

Discussion

We provide evidence that a *C. elegans* cDNA (CeD6.1) encodes a Δ^6 desaturase, and that this sequence is identical with the predicted ORF W08D2.4, except for a 30

residue insertion present in the N-terminal region of the latter protein. Whether the deduced amino acid sequence predicted for CeD6.1 represents a splicing variant of W08D2.4, or is a result of a mis-prediction of the intron/exon junctions by the Genefinder programme is unclear. However it is clear that CeD6.1 encodes a Δ^6 desaturase.

The ORF encoded by the this *C. elegans* sequence appears to be related to the higher plant Δ^6 fatty acid desaturase previously isolated by us [7], in that they both contain N-terminal domains which show homology to cytochrome b_5. Microsomal fatty acid desaturases have been demonstrated to use free microsomal cytochrome b_5 as their electron donor [12, 13], and the vast majority of identified sequences for these enzymes appear not to contain this additional cytochrome b_5 domain [2, 3, 14].

Prior to the present invention only two examples of cytochrome b_5-domain-containing desaturases were known, one being the borage Δ^6 desaturase, and the other being the yeast microsomal Δ^9 (OLE1) desaturase [14, 15]. OLE1, however, contains a C-terminal cytochrome b_5 domain [14, 15]. The reason why these fatty acid desaturases have evolved to contain cytochrome b_5 domains is unclear, though it may be that the Δ^6 desaturase contains this extension as a result of being a "front-end" desaturase. (A "front-end" desaturation can defined as the final desaturation reaction on the fatty acid chain, usually introducing double bonds between the C-3 and C-7 positions from the COOH group [15, 16].)

In any event, it is now believed to be the case that both a variant histidine box and an N-terminal cytochrome b_5 domain are conserved in both animals and plants, as evidenced by their presence in both the borage and nematode Δ^6 desaturases.

This information may therefore allow the identification of other Δ^6 desaturases and also other "front-end" desaturases to be identified by the presence of these motifs.

For reference purposes Figure 5 is provided to show in simplified form a metabolic pathway believed to occur in certain organisms (including humans) and involving Δ^6 desaturases. It can be seen that GLA can be synthesised *in vivo* from linoleic acid under the action of a Δ^6 desaturase and that GLA can be used to synthesise dihomo-GLA, which can be converted to arachidonic acid under the influence of a Δ^5 desaturase. Arachidonic acid is a precursor of various important eicosanoids (including prostaglandins and leucotrienes). Thus it is clear that the Δ^6 desaturase is the first comitted step on the biosynthetic pathway of these biologically active molecules (see Fig. 5).

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Claims

1. A polypeptide having desaturase activity, which:

a) has the amino acid sequence shown in Figure 1

b) has one or more amino acid deletions, insertions or substitutions relative to a polypeptide as defined in a) above, but has at least 32% amino acid sequence identity therewith; or

c) is a fragment of a polypeptide as defined in a) or b) above, which is at least 100 amino acids long.

2. A polypeptide according to claim 1, which has a cytochrome domain

3. A polypeptide according to claim 2, which has a cytochrome b_5 domain

4. A polypeptide according to any preceding claim, which has at least one histidine box.

5. A polypeptide according to any preceding claim, which has three histidine boxes.

6. A polypeptide according to any preceding claim, which is a front end desaturase.

7. A polypeptide according to any preceding claim, which is a Δ^6 desaturase.

8. A polypeptide according to any preceding claim, which occurs naturally in an organism that does not accumulate GLA

9. A polypeptide according to any preceding claim, which occurs naturally in a eukaryote.

10. A polypeptide according to any preceding claim, which occurs naturally in an animal.

11. A polypeptide according to any preceding claim, which occurs naturally in a nematode.

12. A polypeptide according to any preceding claim, which occurs naturally in *C. elegans*.

13. A polypeptide according to claim 1, which consists of the amino acid sequence shown in Figure 1 or of a part thereof.

14. A polypeptide comprising a polypeptide according to any preceding claim, when covalently linked to another moiety.

15. The use of a polypeptide according to any of claims 1 to 14 in raising or selecting antibodies.

16. The use of a polypeptide according to any of claims 1 to 14 as a marker for transformation.

17. The use of a polypeptide according to claim 16 as a marker for plant transformation.

18. An antibody or a derivative thereof which binds to a polypeptide according to any of claims 1 to 14.

19. An antibody or a derivative thereof according to claim 18, for use in diagnosis.

20. A method for assessing whether or not an organism (e.g. a human patient) has a polypeptide according to any of claims 1 to 14, comprising determining whether or not the organism has a polypeptide that binds to an antibody or a derivative thereof according to claim 18.

21. A polypeptide according to any of claims 1 to 14, for use in medicine.

22. The use of a polypeptide according to any of claims 1 to 14 in the preparation of a medicament for treating a disorder involving a deficiency in GLA in a metabolite derived *in vivo* from GLA (e.g. an eicosanoid).

23. The use according to claim 22, wherein the disorder is eczema, mastalgia, hypercholesterolemia, atherosclerosis, coronary disease, diabetic neuropathy, viral infections and cancer.

24. A method of making GLA comprising using a polypeptide according claim 7 to convert linoleic acid to GLA

25. A nucleic acid molecule which:
a) codes for a polypeptide according to any of claims claim 1 to 14,
b) is the complement of a nucleic acid molecule as defined in a) above, or
c) hybridises to a nucleic acid molecule as defined in a) or b) above.

26. A vector comprising a nucleic acid molecule according to claim 25.

27. A non-human host comprising a nucleic acid molecule according to claim 25 or a vector according to claim 26.

28. A host according to claim 27, which is a plant or plant propagating material.

29. A host according to claim 27 or claim 28, which is oil seed rape, sunflower, cereals including maize, tobacco, legumes including peanut and soybean, safflower, oil palm, coconut and other palms, cotton, sesame, mustard, linseed, castor, borage and evening primrose; or which is propagating material for any of the aforesaid.

30. A method for obtaining a polypeptide according to any of claims 1 to 14, comprising incubating a host according to any of claims 27 to 29 under conditions causing expression of said polypeptide and then purifying said polypeptide.

31. The use of nucleic acid molecule according to claim 25 as a probe or as a primer.

32. The use of a nucleic acid molecule according to claim 25 or a vector according to claim 26 for preparing a non-human organism that accumulates GLA or a metabolite derived from GLA in that organism.

33. The use of a nucleic acid molecule according to claim 25 or a vector according to claim 24 for preparing a non-human organism that is chill resistant.

34. A method of producing a non-human host according to any of claims 27 to 29, comprising incorporating a nucleic acid according to claim 25 or a vector according to claim 26 into a non-human organism.

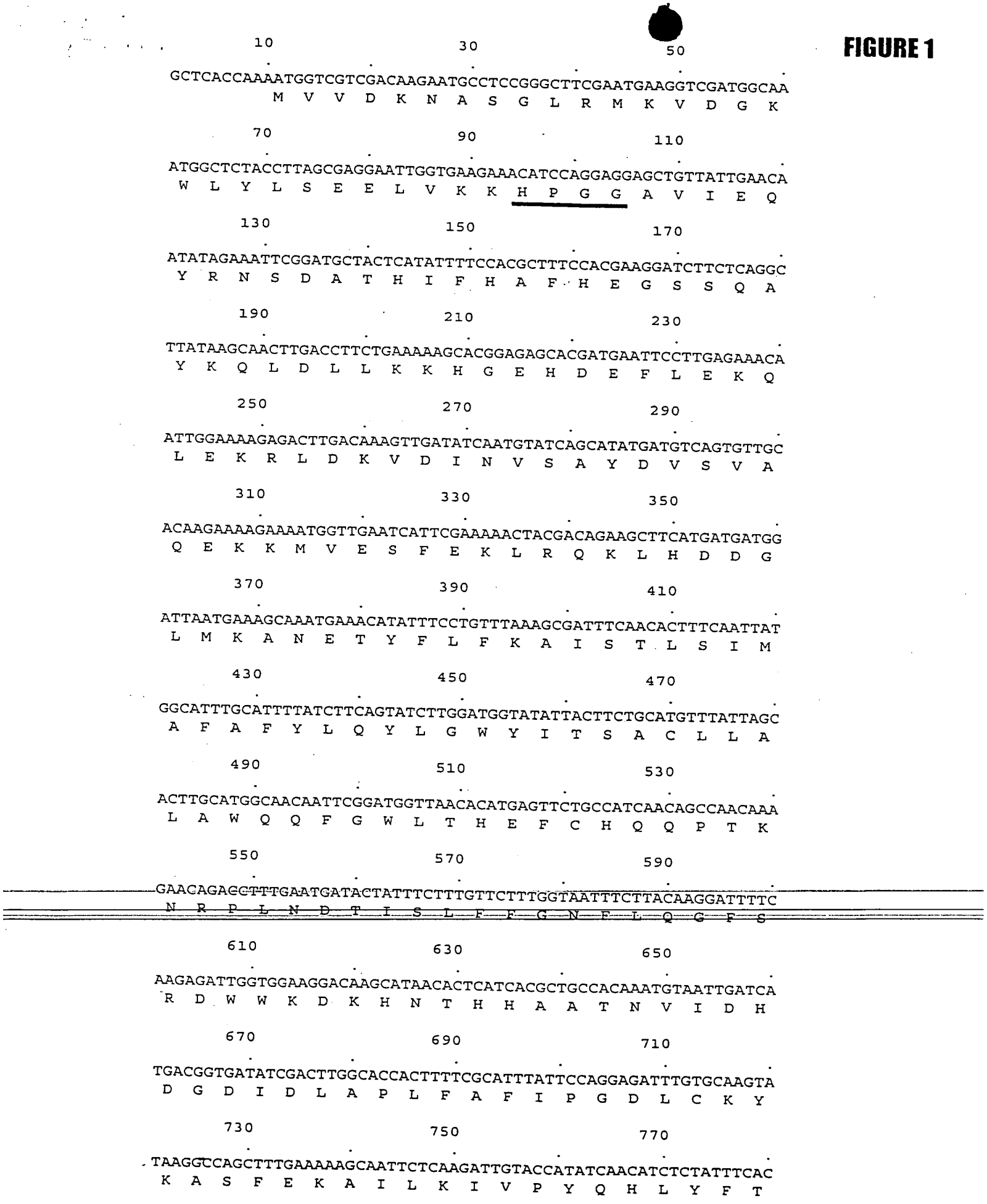
35. The invention as substantially hereinbefore described.

Abstract

Desaturases

cDNA encoding *C. elegans* Δ^6 desaturase has been cloned and sequenced, and the Δ^6 desaturase amino acid sequence has been determined. The *C. elegans* Δ^6 desaturase has a surprisingly low level of sequence identity with the known borage Δ^6 desaturase. The *C. elegans* Δ^6 desaturase has been expressed in yeast. It and other desaturases can be cloned in host organisms (e.g. plants) and can be used to provide useful metabolites.

FIGURE 1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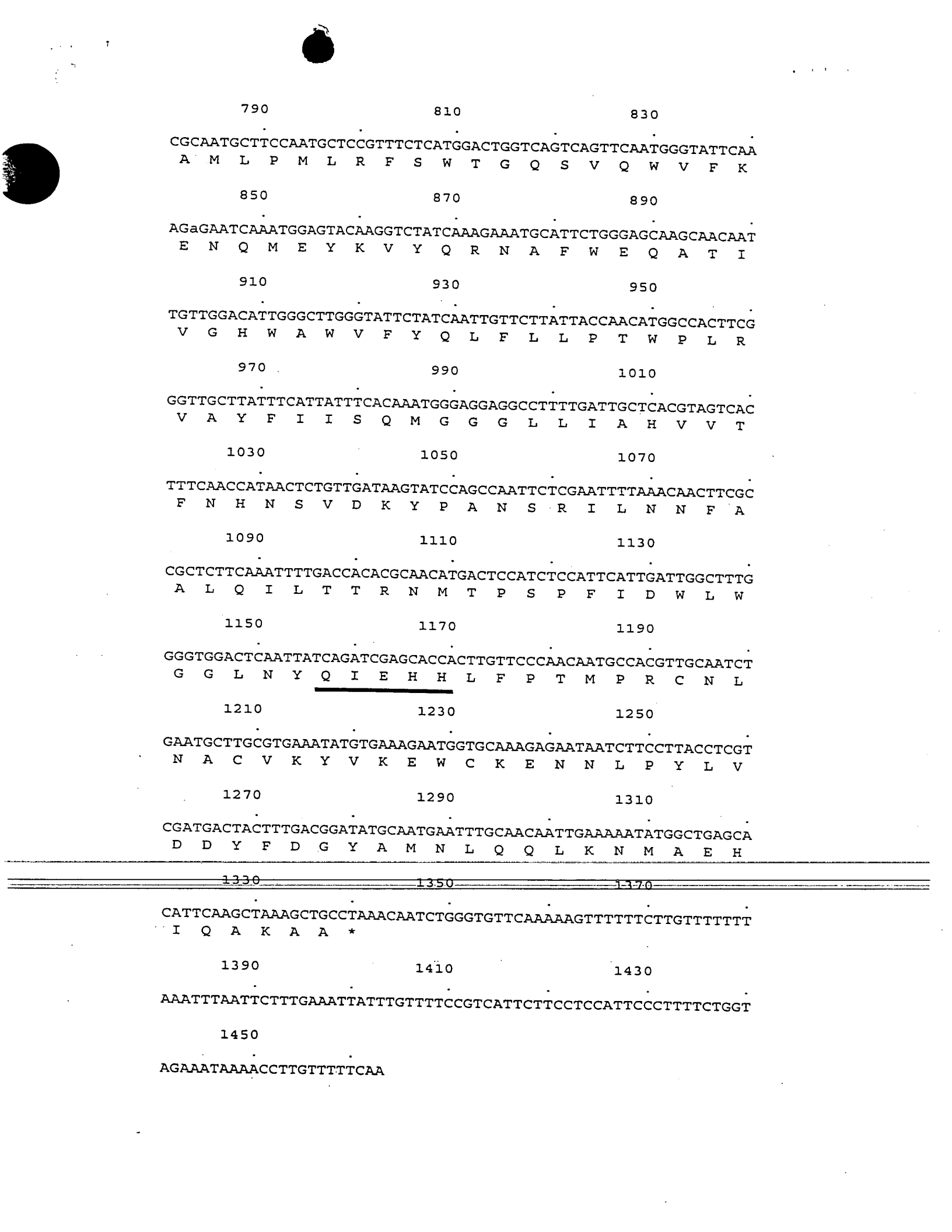
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FIGURE 2A

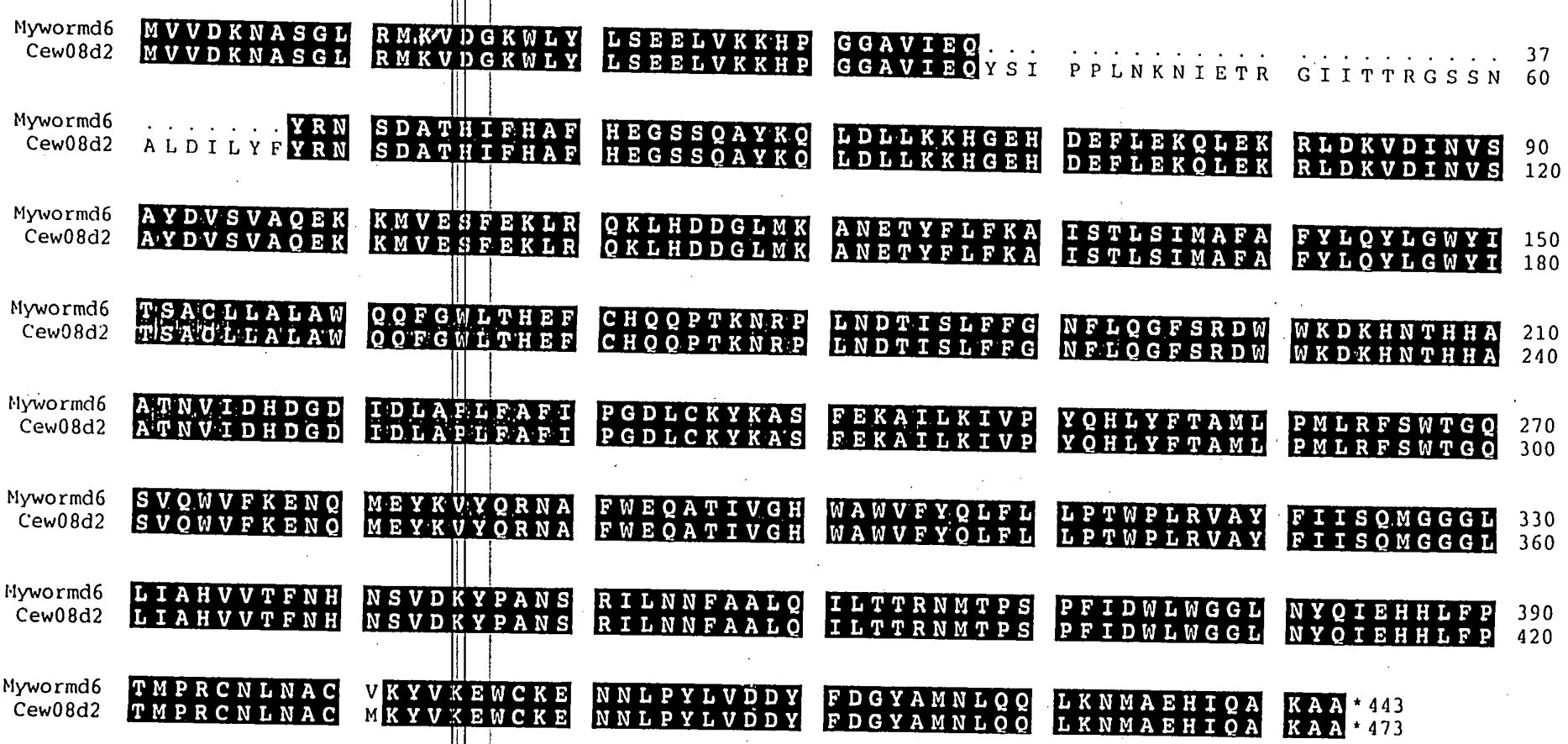
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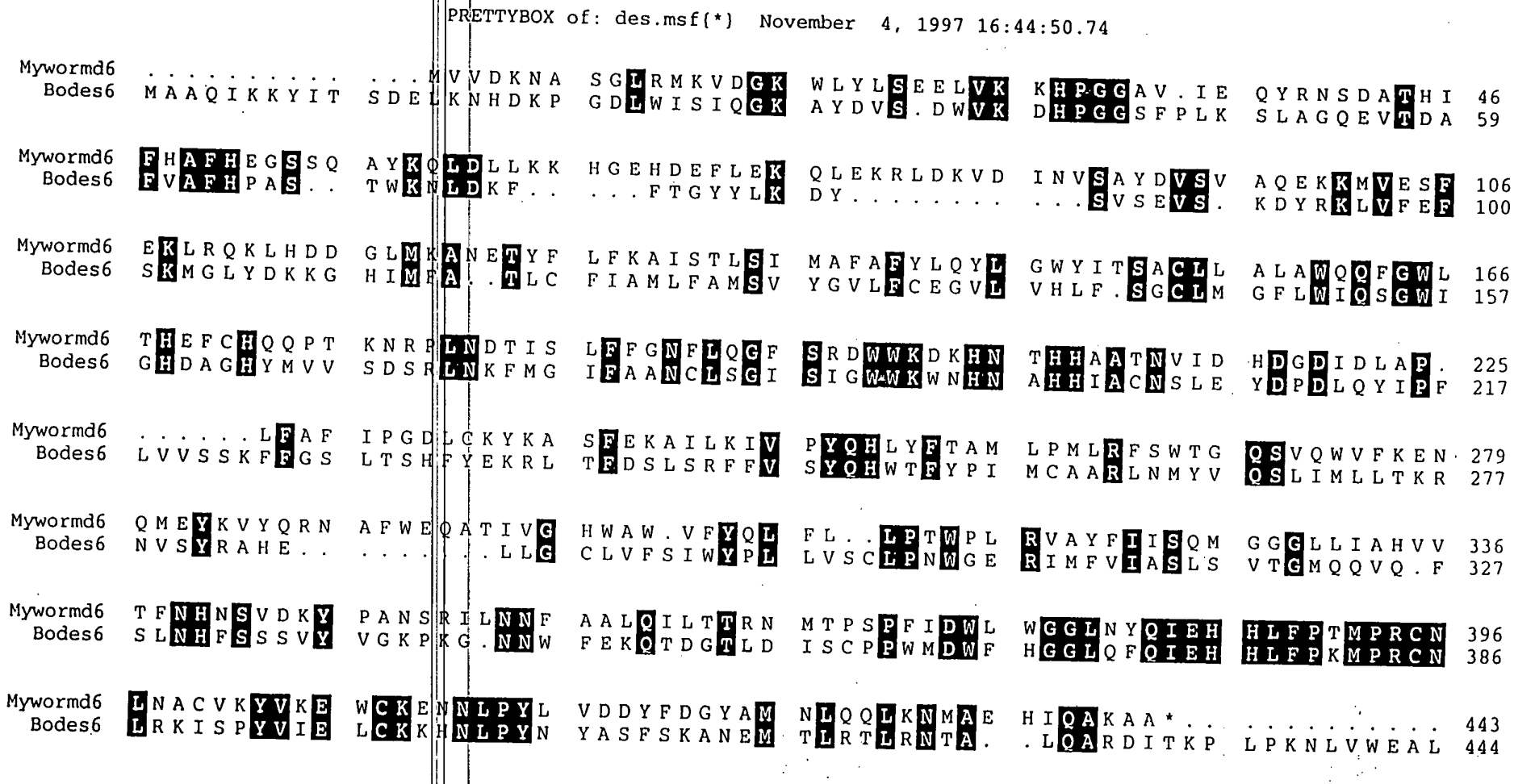
FIGURE 2B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Mywormd6 EKLRQKLHDD GLMKANETYF LFKAISTLSI MAFAFYLQYL GWYITSACLL ALAWQQFGWL 166
Bodes6 SKMGLYDKKG HIMFA..TLC FIAMLFAMSV YGVLFCEGVL VHLF.SGCLM GFLWIQSGWI 157
Mywormd6 THEFCHQQPT KNRPLNDTIS LFFGNFLQGF SRDWWKDKHN THHAATNVID HDGDIDLAP. 225
Bodes6 GHDAGHYMVV SDSRLNKFMG IFAANCLSGI SIGWWKWNHN AHHIACNSLE YDPDLQYIPF 217
Mywormd6 .....LFAF IPGDLCKYKA SFEKAILKIV PYQHLYFTAM LPMLRFSWTG QSVQWVFKEN 279
Bodes6 LVVSSKFFGS LTSHFYEKRL TFDSLSRFFV SYQHWTFYPI MCAARLNMYV QSLIMLLTKR 277
Mywormd6 QMEYKVYQRN AFWEQATIVG HWAW.VFYQL FL..LPTWPL RVAYFISQM GGGLLIAHVV 336
Bodes6 NVSYRAHE.. ....LLG CLVFSIWYPL LVSCLPNWGE RIMFVIASLS VTGMQQVQ.F 327
Mywormd6 TFNHNSVDKY PANSRILNNF AALQILTTRN MTPSPFIDWL WGGLNYQIEH HLFPTMPRCN 396
Bodes6 SLNHFSSSVY VGKPKG.NNW FEKQTDGTLD ISCPPWMDWF HGGLQFQIEH HLFPKMPRCN 386
Mywormd6 LNACVKYVKE WCKENNLPYL VDDYFDGYAM NLQQLKNMAE HIQAKAA*.. 443
Bodes6 LRKISPYVIE LCKKHNLPYN YASFSKANEM TLRTLRNTA. .LQARDITKP LPKNLVWEAL 444
Mywormd6 443
Bodes6 HTHG*448

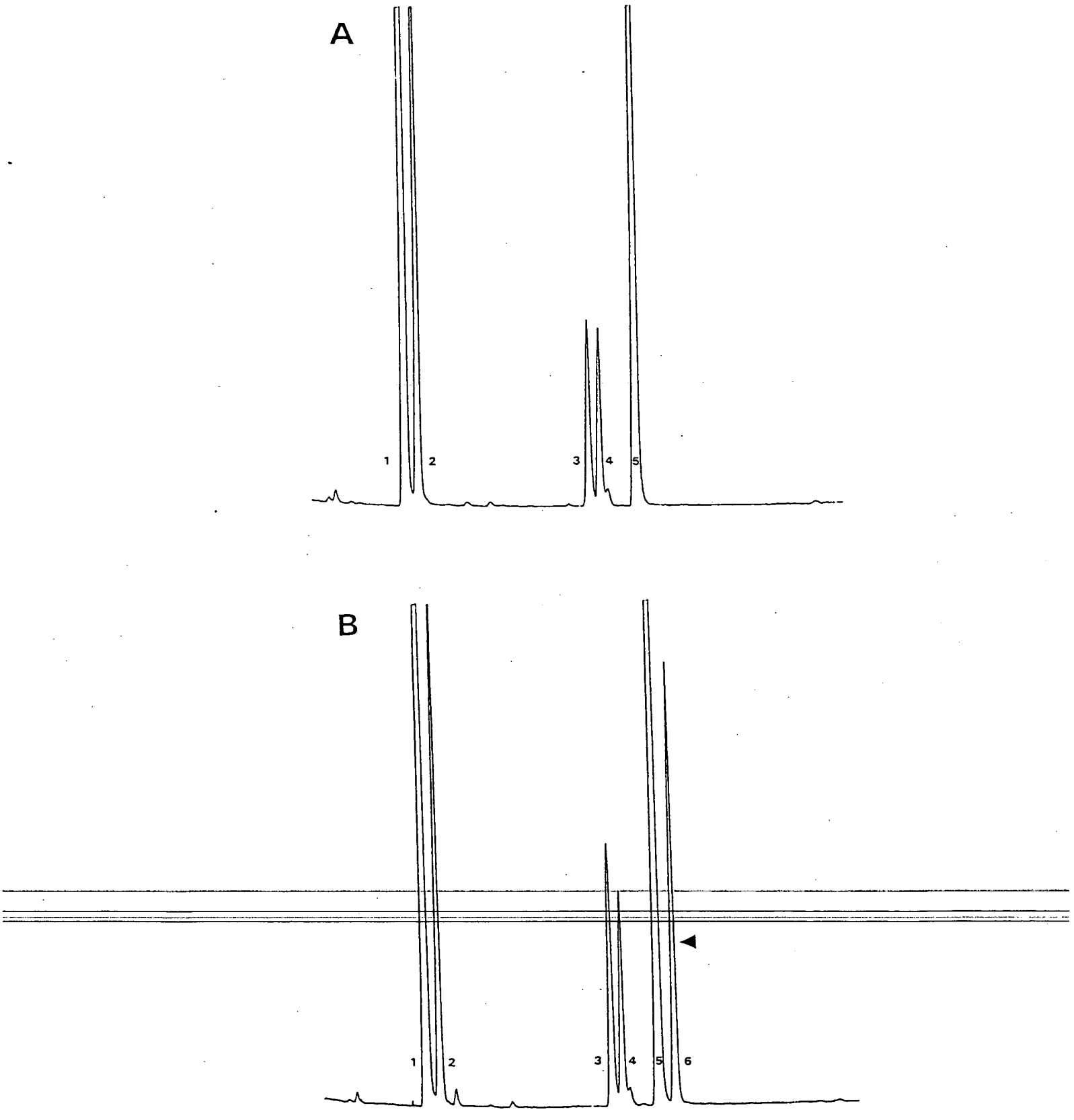


FIGURE 3

FIGURE 4

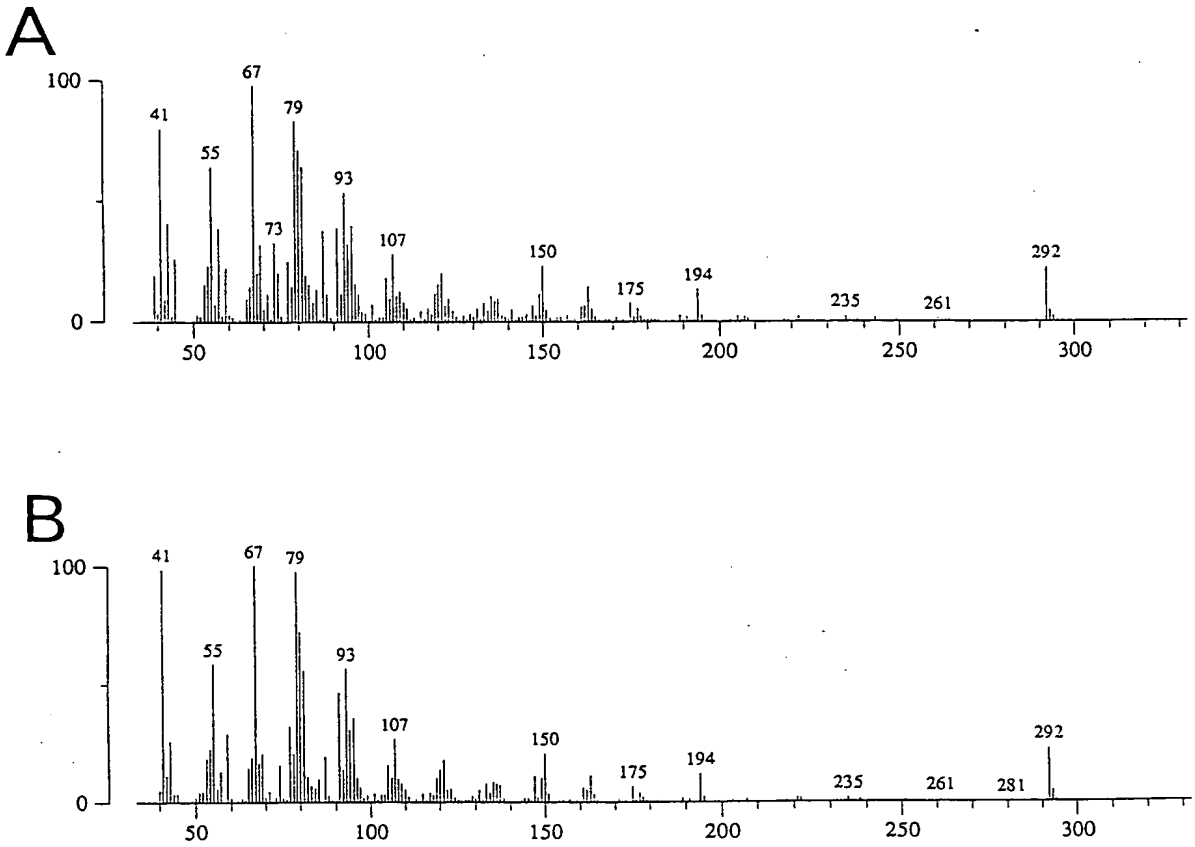
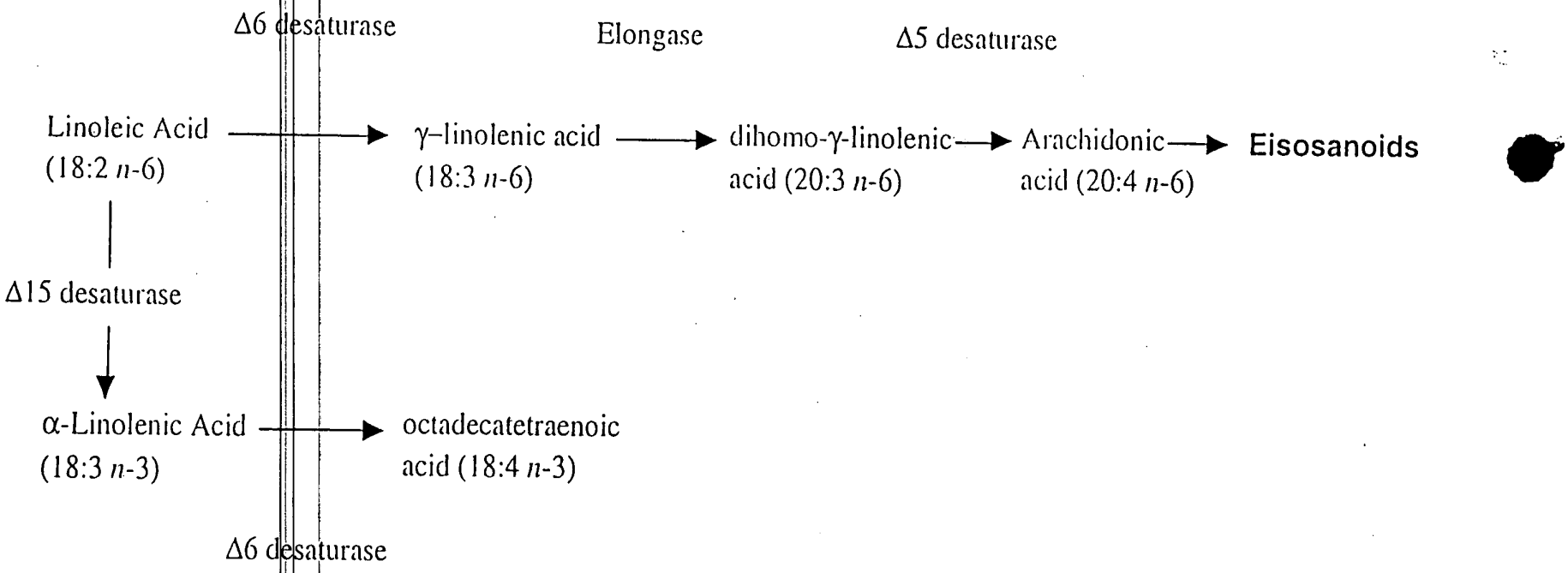

A
100
0
41
55
67
73
79
93
107
150
175
194
235
261
292
50
100
150
200
250
300
B
100
0
41
55
67
79
93
107
150
175
194
235
261
281
292
50
100
150
200
250
300

FIGURE 5


Δ6 desaturase
Elongase
Δ5 desaturase
Linoleic Acid (18:2 n-6)
γ–linolenic acid (18:3 n-6)
dihomo-γ-linolenic acid (20:3 n-6)
Arachidonic acid (20:4 n-6)
Eisosanoids
Δ15 desaturase
α-Linolenic Acid (18:3 n-3)
octadecatetraenoic acid (18:4 n-3)
Δ6 desaturase